

Initial assembled sequence  
[Strand]

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1   AGAAAATACC CACTTTCTCA GGATGATATC AATGGAATCC AGTCCATCTA TGGAGGTCTG
61  CCTAAGGAAC CTGCTAAGCC AAAGGAACCC ACTATACCCC ATGCCTGTGA CCCTGACTTG
121 ACTTTTGACG CTATCACAAC TTTCCGCAGA GAAGTAATGT TCTTTAAAGG CAGGCACCTA
181 TGGAGGATCT ATTATGATAT CACGGATGTT GAGTTTGAAT TAATTGCTTC ATTCTGGCCA
241 TCTCTGCCAG CTGATCTGCA AGCTGCATAC GAGAACCCCA GAGATAAGAT TCTGGTTTTT
301 AAAGATGAAA ACTTCTGGAT GATCAGAGGA TATGCTGTCT TGCCAGATTA TCCCAAATCC
361 ATCCATACAT TAGGTTTTCC AGGACGTGTG AAGAAAATAG ATGCAGCCGT CTGTGATAAG
421 ACCACAAGAA AAACCTACTT CTTTGTGGGC ATTTGGTGCT GGAGGTTTGA TGAAATGACC
481 CAAACCATGG ACAAAGGGTT CCCGCAGAGA GTGGTAAAC ACTTTCCTGG AATCAGTATC
541 CGTGTTGATG CTGCTTTCCA GTACAAAGGA TTCTTCTTTT TCAGCCGTGG ATCAACGCAA
601 TTTGAATACG ACATTAAGAC AAAGAATATT ACCCGAATCA TGAGAACTAA TACTTGGTTT
661 CAATGCAAAG AACCAAAGAA CTCCTCATTT GGTTTTGATA TCAACAAGGA AAAAGCACAT
721 TCAGGAGGCA TAAAGATATT GTATCATAAG AGTTTAAGCT TGTTTATTTT TGGTATTGTT
781 CATTTGCTGA AAAACACTTC TATTTATCAA TAAATTCATA GACCTAAAAT AAA
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Figure 1

gaaagagagg a	atg aag cgc ctt ctg ctt ctg ttt ttg ttc ttt ata aca	50
	<u>Met Lys Arg Leu Leu Leu Phe Leu Phe Phe Ile Thr</u>	
	1 5 10	
ttt tct tct gca ttt ccc tta gtc cgg atg atg gaa aat gaa gaa aat	98	
<u>Phe Ser Ser</u> Ala Phe Pro Leu Val Arg Met Met Glu Asn Glu Glu Asn		
15 20 25		
gtg caa ctg gct cag gca tat ctc aac cag ttc tac tct ctt gaa ata	146	
Val Gln Leu Ala Gln Ala Tyr Leu Asn Gln Phe Tyr Ser Leu Glu Ile		
30 35 40 45		
gaa ggg aat cat ctt gtt caa agc aag aat agg agt ctc ata gat gac	194	
Glu Gly Asn His Leu Val Gln Ser Lys Asn Arg Ser Leu Ile Asp Asp		
50 55 60		
aaa att cgg gaa atg caa gca ttt ttt gga ttg aca gtg act gga aga	242	
Lys Ile Arg Glu Met Gln Ala Phe Phe Gly Leu Thr Val Thr Gly Arg		
65 70 75		
ctg gac tca aac acc ctt gag atc atg aag aca ccc agg tgt ggg gtg	290	
Leu Asp Ser Asn Thr Leu Glu Ile Met Lys Thr <u>Pro Arg Cys Gly Val</u>		
80 85 90		
cct gat gtg ggc cag tat ggc tac acc ctc cct ggg tgg aga aaa tac	338	
<u>Pro Asp</u> Val Gly Gln Tyr Gly Tyr Thr Leu Pro Gly Trp Arg Lys Tyr		
95 100 105		
aac ctc acc tac aga ata ata aac tat act ccg gat atg gca cga gct	386	
Asn Leu Thr Tyr Arg Ile Ile Asn Tyr Thr Pro Asp Met Ala Arg Ala		
110 115 120 125		
gct gtg gat gag gct atc caa gaa ggt tta gaa gtg tgg agc aaa gtc	434	
Ala Val Asp Glu Ala Ile Gln Glu Gly Leu Glu Val Trp Ser Lys Val		
130 135 140		
act cca cta aaa ttc acc aag att tca aag ggg att gca gac atc atg	482	
Thr Pro Leu Lys Phe Thr Lys Ile Ser Lys Gly Ile Ala Asp Ile Met		
145 150 155		
att gcc ttt agg act cga gtc cat ggt cgg tgt cct cgc tat ttt gat	530	
Ile Ala Phe Arg Thr Arg Val His Gly Arg Cys Pro Arg Tyr Phe Asp		
160 165 170		
ggt ccc ttg gga gtt ctt ggc cat gcc ttt cct cct ggt ccg ggt ctg	578	
Gly Pro Leu Gly Val Leu Gly His Ala Phe Pro Pro Gly Pro Gly Leu		
175 180 185		
ggt ggt gac act cat ttt gat gag gat gaa aac tgg acc aag gat gga	626	
Gly Gly Asp Thr His Phe Asp Glu Asp Glu Asn Trp Thr Lys Asp Gly		
190 195 200 205		
gca gga ttc aac ttg ttt ctt gtg gct gct cat gaa ttt ggt cat gca	674	
Ala Gly Phe Asn Leu Phe Leu Val Ala His Glu Phe Gly His Ala		
210 215 220		

**Figure 2A**

ctg ggg ctc tct cac tcc aat gat caa aca gcc ttg atg ttc cca aat	722
Leu Gly Leu Ser His Ser Asn Asp Gln Thr Ala Leu Met Phe Pro Asn	
225 230 235	
tat gtc tcc ctg gat ccc aga aaa tac cca ctt tct cag gat gat atc	770
Tyr Val Ser Leu Asp Pro Arg Lys Tyr Pro Leu Ser Gln Asp Asp Ile	
240 245 250	
aat gga atc cag tcc atc tat gga ggt ctg cct aag gaa cct gct aag	818
Asn Gly Ile Gln Ser Ile Tyr Gly Gly Leu Pro Lys Glu Pro Ala Lys	
255 260 265	
cca aag gaa ccc act ata ccc cat gcc tgt gac cct gac ttg act ttt	866
Pro Lys Glu Pro Thr Ile Pro His Ala Cys Asp Pro Asp Leu Thr Phe	
270 275 280 285	
gac gct atc aca act ttc cgc aga gaa gta atg ttc ttt aaa ggc agg	914
Asp Ala Ile Thr Thr Phe Arg Arg Glu Val Met Phe Phe Lys Gly Arg	
290 295 300	
cac cta tgg agg atc tat tat gat atc acg gat gtt gag ttt gaa tta	962
His Leu Trp Arg Ile Tyr Tyr Asp Ile Thr Asp Val Glu Phe Glu Leu	
305 310 315	
att gct tca ttc tgg cca tct ctg cca gct gat ctg caa gct gca tac	1010
Ile Ala Ser Phe Trp Pro Ser Leu Pro Ala Asp Leu Gln Ala Ala Tyr	
320 325 330	
gag aac ccc aga gat aag att ctg gtt ttt aaa gat gaa aac ttc tgg	1058
Glu Asn Pro Arg Asp Lys Ile Leu Val Phe Lys Asp Glu Asn Phe Trp	
335 340 345	
atg atc aga gga tat gct gtc ttg cca gat tat ccc aaa tcc atc cat	1106
Met Ile Arg Gly Tyr Ala Val Leu Pro Asp Tyr Pro Lys Ser Ile His	
350 355 360 365	
aca tta ggt ttt cca gga cgt gtg aag aaa ata gat gca gcc gtc tgt	1154
Thr Leu Gly Phe Pro Gly Arg Val Lys Lys Ile Asp Ala Ala Val Cys	
370 375 380	
gat aag acc aca aga aaa acc tac ttc ttt gtg ggc att tgg tgc tgg	1202
Asp Lys Thr Thr Arg Lys Thr Tyr Phe Phe Val Gly Ile Trp Cys Trp	
385 390 395	
agg ttt gat gaa atg acc caa acc atg gac aaa ggg ttc ccg cag aga	1250
Arg Phe Asp Glu Met Thr Gln Thr Met Asp Lys Gly Phe Pro Gln Arg	
400 405 410	
gtg gta aaa cac ttt cct gga atc agt atc cgt gtt gat gct gct ttc	1298
Val Val Lys His Phe Pro Gly Ile Ser Ile Arg Val Asp Ala Ala Phe	
415 420 425	
cag tac aaa gga ttc ttc ttt ttc agc cgt gga tca acg caa ttt gaa	1346
Gln Tyr Lys Gly Phe Phe Phe Phe Ser Arg Gly Ser Thr Gln Phe Glu	
430 435 440 445	

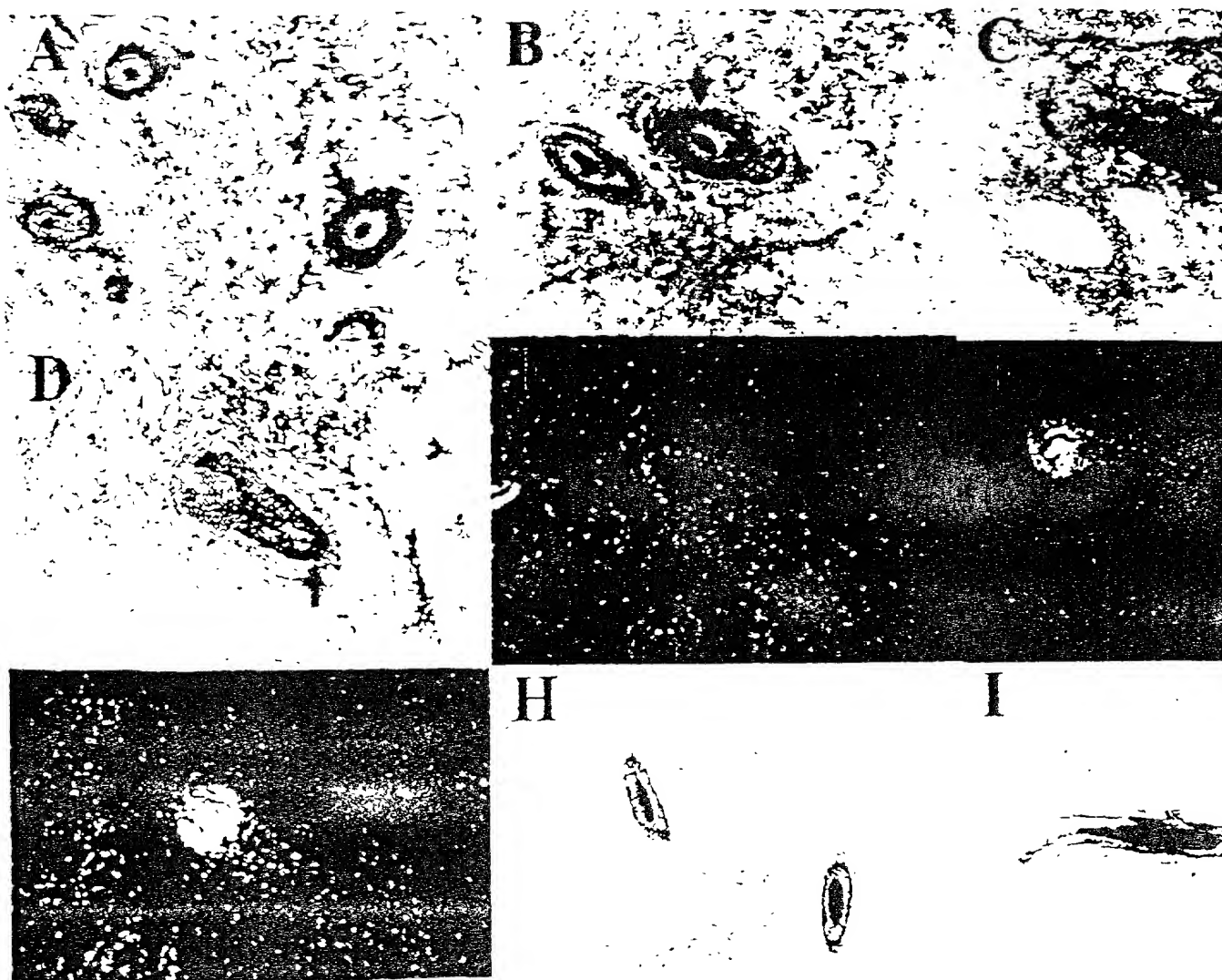
**Figure 2B**

tac gac att aag aca aag aat att acc cga atc atg aga act aat act	1394
Tyr Asp Ile Lys Thr Lys Asn Ile Thr Arg Ile Met Arg Thr Asn Thr	
450 455 460	
tgg ttt caa tgc aaa gaa cca aag aac tcc tca ttt ggt ttt gat atc	1442
Trp Phe Gln Cys Lys Glu Pro Lys Asn Ser Ser Phe Gly Phe Asp Ile	
465 470 475	
aac aag gaa aaa gca cat tca gga ggc ata aag ata ttg tat cat aag	1490
Asn Lys Glu Lys Ala His Ser Gly Gly Ile Lys Ile Leu Tyr His Lys	
480 485 490	
agt tta agc ttg ttt att ttt ggt att gtt cat ttg ctg aaa aac act	1538
Ser Leu Ser Leu Phe Ile Phe Gly Ile Val His Leu Leu Lys Asn Thr	
495 500 505	
tct att tat caa taaattcata gacctaaaat aaacctcaac aggtctttta	1590
Ser Ile Tyr Gln	
510	
atataaatc tgcttcaaaa tagaataaaa ccattcttta acaacaagtt gctggtccta	1650
gttctaaata tccaaattca atggccattt tgagctgcct gattctttta ataggaagtt	1710
attatgtaga aacaaaaatc tctgactgta cttaagcct atttcattgct ttgtggactt	1770
ggagaagaca tgtcttataa ctgaatactg aaacatttat <u>taa</u> ccaatc tttagcattc	1830
tg	1832

**Figure 2C**

[illegible]

[illegible][illegible]



A-G: Antisense RNA probe for human MMP 25

H and I: Sense RNA probe for human MMP 25

Arrows in A, B, C, and D highlight cells in the hair follicle that express MMP25 message

Cell nuclei are counterstained with H33258 in E, F, and G.

Figure 5